

HIGH RESOLUTION ION MOBILITY TANDEM MASS SPECTROMETRY

WATERS GMBH, SYNAPT G2-S

High resolution tandem mass spectrometer equipped with ion mobility cell is used for identification and determination of compounds. The mass spectrometer operates in wide range of molecular masses and polarity and allows measurement of exact value of mass to charge ratio (m/z) of molecular ion of analyzed compound, its fragments (measurement of their m/z values after dissociation of molecular ion in collision cell) and mobility of both parent ions and fragments. The ion mobility measurement allows determination of collision cross section of studied ions which depends on their size and shape. The mass spectrometer is used as standalone or in a combination with two-dimensional ultra-performance liquid chromatography. Mass spectrometric imaging experiments are possible in combination with laser desorption-ionization as well.

ACQUIRED INFORMATION

- > Exact molecular mass of analyzed compound and its fragments
- > Ion mobility and collision cross section values of ions
- > Spatial distribution of molecules on the sample surface
- > Retention characteristics in case of hyphenation of mass spectrometer with liquid chromatography
- > Content of analytes in studied sample

SAMPLE TYPES

- > Liquids and solutions of analytes
- > Solid materials fixed on MALDI plate
- > Clinical and environmental samples, plant extracts
- > Direct analysis of human, animal and plant tissues
- > Characterization of newly synthesized materials

MODES, CONDITIONS AND PRECISION

Used ion sources:

- > Electrospray, atmospheric pressure chemical ionization
- > Laser desorption ionization (with imaging capability)

Analyzer:

- > Hybrid quadrupole-time of flight with integrated mobility cell

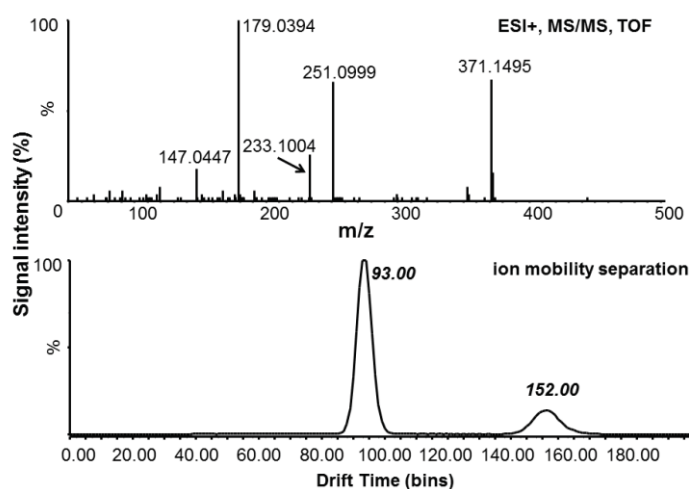
Detector:

- > Ultra-fast electron multiplier in combination with hybrid ADC electronics

Resolution:

- > Up to 40000 (FWHM, according to specification for high resolution mode)

DETAILED INFORMATION ON REQUEST



Fragmentation mass spectrum and ion mobility separation record of selected analytes.



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